

Applicant: Garvan Institute of Medical Research
Title of Invention: NPY-Y7 Receptor Gene

Prior Application Number: PP 4385
Prior Application Filing Date: 1998-06-29

Number of SEQ ID NOs: 5

Software: PatentIn Ver. 2.1

SEQ ID NO: 1
Length: 14
Type: PRT
Organism: Artificial Sequence

Other Information: Description of Artificial Sequence: N-terminal consensus sequence

Sequence: 1
Met Xaa Xaa Met Xaa Glu Lys Trp Asp Xaa Asn Ser Ser Glu
1 5 10

SEQ ID NO: 2
Length: 408
Type: PRT
Organism: Homo sapiens

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Sequence:  2
Met Phe Ile Met Asn Glu Lys Trp Asp Thr Asn Ser Ser Glu Asn Trp
  1             5             10             15
His Pro Ile Trp Asn Val Asn Asp Thr Lys His His Leu Tyr Ser Asp
      20             25             30
Ile Asn Ile Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala
      35             40             45
Ala Ile Phe Ile Ile Ser Tyr Phe Leu Ile Phe Phe Leu Cys Met Met

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50					55					60						
Gly	Asn	Thr	Val	Val	Cys	Phe	Ile	Val	Met	Arg	Asn	Lys	His	Met	His	
65					70				75				80			
Thr	Val	Thr	Asn	Leu	Phe	Ile	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Leu	Leu	
85					90					95						
Val	Gly	Ile	Phe	Cys	Met	Pro	Ile	Thr	Leu	Leu	Asp	Asn	Ile	Ile	Ala	
100				105				110								
Gly	Trp	Pro	Phe	Gly	Asn	Thr	Met	Cys	Lys	Ile	Ser	Gly	Leu	Val	Gln	
115			120			125										
Gly	Ile	Ser	Val	Ala	Ala	Ser	Val	Phe	Thr	Leu	Val	Ala	Ile	Ala	Val	
130		135		140												
Asp	Arg	Phe	Gln	Cys	Val	Val	Tyr	Pro	Phe	Lys	Pro	Lys	Leu	Thr	Ile	
145	150				155				160							
Lys	Thr	Ala	Phe	Val	Ile	Ile	Met	Ile	Ile	Trp	Val	Leu	Ala	Ile	Thr	
165					170					175						
Ile	Met	Ser	Pro	Ser	Ala	Val	Met	Leu	His	Val	Gln	Glu	Glu	Lys	Tyr	
180				185				190								
Tyr	Arg	Val	Arg	Leu	Asn	Ser	Gln	Asn	Lys	Thr	Ser	Pro	Val	Tyr	Trp	
195		200		205												
Cys	Arg	Glu	Asp	Trp	Pro	Asn	Gln	Glu	Met	Arg	Lys	Ile	Tyr	Thr	Thr	
210		215		220												
Val	Leu	Phe	Ala	Asn	Ile	Tyr	Leu	Ala	Pro	Leu	Ser	Leu	Ile	Val	Ile	
225	230				235				240							
Met	Tyr	Gly	Arg	Ile	Gly	Ile	Ser	Leu	Phe	Arg	Ala	Ala	Val	Pro	His	
245					250					255						
Thr	Gly	Arg	Lys	Asn	Gln	Glu	Gln	Trp	His	Val	Val	Ser	Arg	Lys	Lys	
260			265			270										
Gln	Lys	Ile	Ile	Lys	Met	Leu	Leu	Ile	Val	Ala	Leu	Leu	Phe	Ile	Leu	
275		280		285												
Ser	Trp	Leu	Pro	Leu	Trp	Thr	Leu	Met	Met	Leu	Ser	Asp	Tyr	Ala	Asp	
290		295		300												
Leu	Ser	Pro	Asn	Glu	Leu	Gln	Ile	Ile	Asn	Ile	Tyr	Ile	Tyr	Pro	Phe	
305	310				315				320							
Ala	His	Trp	Leu	Ala	Phe	Gly	Asn	Ser	Ser	Val	Asn	Pro	Ile	Ile	Tyr	
325					330					335						
Gly	Phe	Phe	Asn	Glu	Asn	Phe	Arg	Arg	Gly	Phe	Gln	Glu	Ala	Phe	Gln	
340			345			350										
Leu	Gln	Leu	Cys	Gln	Lys	Arg	Ala	Lys	Pro	Met	Glu	Ala	Tyr	Thr	Leu	
355		360		365												

Lys Ala Lys Ser His Val Leu Ile Asn Thr Ser Asn Gln Leu Val Gln
370 375 380
Glu Ser Thr Phe Gln Asn Pro His Gly Glu Thr Leu Leu Tyr Arg Lys
385 390 395 400
Ser Ala Glu Asn Pro Asn Arg Asn
405

SEQ ID NO: 3
Length: 405
Type: PRT
Organism: Mus musculus

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Sequence: 3
Met Ser Thr Met Ser Glu Lys Trp Asp Ser Asn Ser Ser Glu Ser Trp
1          5          10          15
Asn His Ile Trp Ser Gly Asn Asp Thr Gln His His Trp Tyr Ser Asp
20          25          30
Ile Asn Ile Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala
35          40          45
Ala Val Phe Ile Ser Ser Tyr Leu Leu Ile Phe Val Leu Cys Met Val
50          55          60
Gly Asn Thr Val Val Cys Phe Ile Val Ile Arg Asn Arg His Met His
65          70          75          80
Thr Val Thr Asn Phe Leu Ile Leu Asn Leu Ala Ile Ser Asp Leu Leu
85          90          95
Val Gly Ile Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile Ile Ala
100          105          110
Gly Trp Pro Phe Gly Ser Ser Met Cys Lys Ile Ser Gly Leu Val Gln
115          120          125
Gly Ile Ser Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val
130          135          140
Asp Arg Phe Arg Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Val
145          150          155          160
Lys Thr Ala Phe Val Thr Ile Val Ile Ile Trp Gly Leu Ala Ile Ala
165          170          175
Ile Met Thr Pro Ser Ala Ile Met Leu His Val Gln Glu Glu Lys Tyr
180          185          190
Tyr Arg Val Arg Leu Ser Ser His Asn Lys Thr Ser Thr Val Tyr Trp

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SEQ ID NO: 4
Length: 1903
Type: DNA
Organism: Homo sapiens

ctcgagatcc atttggtctt aaaggcctcc tgagtagctg ggactacagg cgcccgccac 60
cacgcttggc taattttttt gtatttttag tagggacggc gtttcactgt gttagccaga 120
tggtctccat ctcccgacct cgtgatccac ccacctcggc ctcccaaagt gctgggatta 180

caggcgtgag accgcgcccg gccaatcttc tttcttagtt gcctctgccc acctcttctc 240
ttctgcttcc atattacagg tttcctcagt tgcgaaatta ggatgtttaa tatagctttt 300
gacatacaag aaacatcaaa aagattgaat gtcttaataa gagtgaagca tgtagatcag 360
tgactgctat gttcatcatg aatgagaaat gggacacaaa ctcttcagaa aactggcatc 420
ccatctggaa tgtcaatgac acaaagcatc atctgtactc agatattaat attacctatg 480
tgaactacta tcttcaccag cctcaagtgg cagcaatctt cattatttcc tacttttctga 540
tcttcttttt gtgcatgatg ggaaatactg tggtttgctt tattgtaatg aggaacaaac 600
atatgcacac agtcactaat ctcttcacat taaacctggc cataagtgat ttactagttg 660
gcatattctg catgcctata aactgctgg acaatattat agcaggatgg ccatctggaa 720
acacgatgtg caagatcagt ggattgggcc agggaaatct tgtcgcagct tcagtcttta 780
cgtaggttgc aattgctgta gatagggttc agtgtgtggt ctacctttt aaaccaaaagc 840
tcactatcaa gacagcgttt gtcattatta tgatcatctg ggtcctagcc atcaccatta 900
tgtctccatc tgcagtaatg ttacatgtgc aagaagaaaa atattaccga gtgagactca 960
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catctaatac gcttgtccag gaatctacat ttcaaaaccc tcatggggaa accttgcttt 1560
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taaaacattt actgaaagcc ctctctggca aaaaaattaa aaataaaca aaatgggtcat 1800
aagatcataa acaatcttat gttgtataaa aatacgtaga gtgacttaga catgtttgca 1860
tgaataaata tatttctaga gaacagttaa aaaaaaaaaa aaa 1903

SEQ ID NO: 5

Length: 1228

Type: DNA

Organism: Mus musculus

091908 120900

Sequence: 5

atgtccacca tgagcyagaa atgggactca aactcttcag aaagctggaa tcacatctgg 60
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tatctccacc agccccaagt ggcagctgtc ttcatacagct cctacctcct gatctttgtc 180
ttgtgcatgg tgggaaatac tgtcgtttgc tttattgtga taaggaatag acacatgcac 240
acagtcaacta atttcttgat cttaaaccct gccataagtg atttactggt tggaatatcc 300
tgtatgccta tcacattgct ggacaacatc atagcaggat ggccattcgg aagcagcatg 360
tgcaagatca gtgggctggt gcaagggata tcagttgcgg ctccgtctt caccttggtt 420
gcaatagctg tggacagatt ccgtgtgtg gtctaccctt ttaagccaaa gctcactgtc 480
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tctgcaataa tgttacatgt acaagaagaa aaatactacc gtgtgagact cagctccac 600
aataaaaacca gcacagtcta ctggtgtcgg gaggactggc caagacacga aatgaggagg 660
atctatacca cgggtgctatt tgccatcatc tatcttgctc ctctctcact cattgttate 720
atgtatgcaa ggattggggc ttccctcttc aagacggcag cacactgcac aggcaagcag 780
cgtccagtgc agtgcattgta tcaagagaaa cagaaggcca tcaagatgct gctgactgtg 840
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ccacacagga atccttgata gaggaatg 1228

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